

Abstract

<120> Novel fructosyltransferases

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<150> 01200049.3

<160> 26

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<212> PRT

<220>

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$$\langle 222 \rangle \quad (5\bar{1}\bar{1})$$
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<221> ACT_SITE
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 <223> Putative catalytic amino acid residue

 <220>
 <221> ACT_SITE
 <222> (551)
 <223> Putative catalytic amino acid residue

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 <222> (1)..(21)
 <223> Putative signal sequence

 <220>
 <221> DOMAIN
 <222> (755)..(759)
 <223> Putative cell wall anchor amino acid signal

<220>
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 <222> (690)..(749)
 <223> PXX repeat (20 -fold)

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 35 40 45
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 Ala Ser Asp Thr Thr Ile Arg Thr Ser Ala Asn Ala Asn Ser Ala Ser
 65 70 75 80
 Ser Ala Ala Asn Thr Gln Asn Ser Asn Ser Gln Val Ala Ser Ser Ala
 85 90 95
 Ala Ile Thr Ser Ser Thr Ser Ser Ala Ala Ser Leu Asn Asn Thr Asp
 100 105 110
 Ser Lys Ala Ala Gln Glu Asn Thr Asn Thr Ala Lys Asn Asp Asp Thr
 115 120 125
 Gln Lys Ala Ala Pro Ala Asn Glu Ser Ser Glu Ala Lys Asn Glu Pro
 130 135 140
 Ala Val Asn Val Asn Asp Ser Ser Ala Ala Lys Asn Asp Asp Gln Gln
 145 150 155 160
 Ser Ser Lys Lys Asn Thr Thr Ala Lys Leu Asn Lys Asp Ala Glu Asn
 165 170 175

Val	Val	Lys	Lys	Ala	Gly	Ile	Asp	Pro	Asn	Ser	Leu	Thr	Asp	Gln	
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<212> DNA
<213> Lactobacillus reuteri

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<211> 2394
<212> DNA

<213> *Lactobacillus reuteri*

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<210> 4

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<212> DNA

<213> *Lactobacillus reuteri*

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<221> RBS

<222> (29)..(32)

<220>

<221> RBS

<222> (54)..(57)

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 <222> (1)..(67)
 <223> Putative expression-regulating region
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 <213> Lactobacillus reuteri

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<213> *Lactobacillus reuteri*

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<220>
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15 20 25	
gct gat caa gta gaa agt aac aat tac aac ggt gtt gct gaa gtt aat	1348
Ala Asp Gln Val Glu Ser Asn Asn Tyr Asn Gly Val Ala Glu Val Asn	
30 35 40	
act gaa cgt caa gct aat ggt caa att ggc gta gat gga aaa att att	1396
Thr Glu Arg Gln Ala Asn Gly Gln Ile Gly Val Asp Gly Lys Ile Ile	
45 50 55	
agt gct aac agt aat aca acc agt ggc tgc aca aat caa gaa tca tct	1444
Ser Ala Asn Ser Asn Thr Thr Ser Gly Ser Thr Asn Gln Glu Ser Ser	
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aac aat act gaa aat gct gtt gtt aat gaa aac aaa aat act aac aat	1540
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110 115 120	
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175 180 185	
aaa ttg acc ttt aag gac tta gag ggg att ggt aat gct att gtt aag	1828
Lys Leu Thr Phe Lys Asp Leu Glu Gly Ile Gly Asn Ala Ile Val Lys	
190 195 200	
caa gat cca caa tat gct att cct tat tct aat gct aag gaa atc aag	1876
Gln Asp Pro Gln Tyr Ala Ile Pro Tyr Ser Asn Ala Lys Glu Ile Lys	
205 210 215	

ttc Phe	aag Lys 445	ctt Leu	ttg Leu	aat Asn	aat Asn	aag Lys 450	aag Lys	gat Asp	cgt Arg	gaa Glu	ttg Leu 455	gct Ala	ggt Gly	tta Leu	gct Ala	2596
aat Asn 460	ggt Gly	gca Ala	ctt Leu	ggt Gly	atc Ile 465	tta Leu	aag Lys	ctc Leu	act Thr	aac Asn 470	aat Asn	caa Gln	agt Ser	aag Lys	cca Pro 475	2644
aag Lys	gtt Val	gaa Glu	gaa Glu	gta Val 480	tac Tyr	tca Ser	cca Pro	ttg Leu	gta Val 485	tct Ser	act Thr	ttg Leu	atg Met	gct Ala 490	tgc Cys	2692
gat Asp	gag Glu	gta Val	nnn Xaa 495	nnn Xaa	aag Lys	ctt Leu	ggt Gly	gat Asp 500	aag Lys	tat Tyr	tat Tyr	ctc Leu	ttc Phe 505	tcc Ser	gta Val	2740
act Thr	cgt Arg	gta Val 510	agt Ser	cgt Arg	ggt Gly	tcc Ser	gat Asp 515	cgt Arg	gaa Glu	tta Leu	acc Thr 520	gct Ala	aag Lys	gat Asp	aac Asn	2788
aca Thr	atc Ile 525	gtt Val	ggt Gly	gat Asp	aac Asn 530	gtt Val	gct Ala	atg Met	att Ile	ggt Gly	tac Tyr 535	gtt Val	tcc Ser	gat Asp	agc Ser	2836
tta Leu 540	atg Met	ggt Gly	aag Lys	tac Tyr	aag Lys 545	cca Pro	tta Leu	aat Asn	aac Asn	tca Ser 550	ggt Gly	gtc Val	gta Val	tta Leu	act Thr 555	2884
gca Ala	tca Ser	gta Val	cct Pro	gca Ala 560	aac Asn	tgg Trp	cgt Arg	act Thr	gct Ala 565	act Thr	tat Tyr	tcc Ser	tac Tyr	tat Tyr 570	gca Ala	2932
gta Val	cct Pro	gta Val	gct Ala 575	ggt Gly	cat His	cct Pro	gat Asp	caa Gln 580	gta Val	tta Leu	att Ile	act Thr 585	tct Ser	tac Tyr	atg Met	2980
agt Ser	aac Asn	aag Lys 590	gac Asp	ttt Phe	gct Ala	tca Ser	ggt Gly 595	gaa Glu	gga Gly	aac Asn	tat Tyr 600	gca Ala	act Thr	tgg Trp	gca Ala	3028
cca Pro	agt Ser 605	ttc Phe	tta Leu	gta Val	caa Gln	atc Ile 610	aat Asn	cca Pro	gat Asp	gac Asp	acg Thr 615	aca Thr	act Thr	gta Val	tta Leu	3076
gca Ala 620	cgt Arg	gca Ala	act Thr	aac Asn	caa Gln 625	ggt Gly	gac Asp	tgg Trp	gtg Val	tgg Trp 630	gac Asp	gac Asp	tct Ser	agt Ser	cgg Arg 635	3124
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gcc Ala	tta Leu	cca Pro	ggt Gly 655	gaa Glu	tgg Trp	ggt Gly	aag Lys	cca Pro 660	gtt Val	gac Asp	tgg Trp	agt Ser	ttg Leu 665	att Ile	aac Asn	3220
aga	agt	cct	ggc	tta	ggc	tta	aag	cct	cat	caa	cca	gtt	caa	cca	aag	3268

Arg	Ser	Pro	Gly	Leu	Gly	Leu	Lys	Pro	His	Gln	Pro	Val	Gln	Pro	Lys	
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att	gat	caa	cct	gat	caa	caa	cct	tct	ggt	caa	aac	act	aag	aat	gtc	3316
Ile	Asp	Gln	Pro	Asp	Gln	Gln	Pro	Ser	Gly	Gln	Asn	Thr	Lys	Asn	Val	
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aca	cca	ggt	aat	ggt	gat	aag	cct	gct	ggt	aag	gca	act	cct	gat	aac	3364
Thr	Pro	Gly	Asn	Gly	Asp	Lys	Pro	Ala	Gly	Lys	Ala	Thr	Pro	Asp	Asn	
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act	aat	att	gat	cca	agt	gca	caa	cct	tct	ggt	caa	aac	act	aat	att	3412
Thr	Asn	Ile	Asp	Pro	Ser	Ala	Gln	Pro	Ser	Gly	Gln	Asn	Thr	Asn	Ile	
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gat	cca	agt	gca	caa	mct	tct	ggt	caa	aac	act	aag	aat	gtc	aca	cca	3460
Asp	Pro	Ser	Ala	Gln	Xaa	Ser	Gly	Gln	Asn	Thr	Lys	Asn	Val	Thr	Pro	
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Gly	Asn	Glu	Lys	Gln	Gly	Lys	Asn	Thr	Asp	Ala	Lys	Gln	Leu	Pro	Gln	
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aca	ggt	aat	aag	tct	ggt	tta	gca	gga	ctt	tac	gct	ggt	tca	tta	ctt	3556
Thr	Gly	Asn	Lys	Ser	Gly	Leu	Ala	Gly	Leu	Tyr	Ala	Gly	Ser	Leu	Leu	
	765					770				775						
gcc	ttg	ttt	gga	ttg	gca	gca	att	gaa	aag	cgt	cac	gct	taa			3598
Ala	Leu	Phe	Gly	Leu	Ala	Ala	Ile	Glu	Lys	Arg	His	Ala				
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			20					25					30		
Ser	Asn	Asn	Tyr	Asn	Gly	Val	Ala	Glu	Val	Asn	Thr	Glu	Arg	Gln	Ala
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Asn	Gly	Gln	Ile	Gly	Val	Asp	Gly	Lys	Ile	Ile	Ser	Ala	Asn	Ser	Asn
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Thr	Thr	Ser	Gly	Ser	Thr	Asn	Gln	Glu	Ser	Ser	Ala	Thr	Asn	Asn	Thr
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Glu	Asn	Ala	Val	Val	Asn	Glu	Ser	Lys	Asn	Thr	Asn	Asn	Thr	Glu	Asn
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Ala	Val	Val	Asn	Glu	Asn	Lys	Asn	Thr	Asn	Asn	Thr	Glu	Asn	Ala	Val
			100					105					110		
Val	Asn	Glu	Asn	Lys	Asn	Thr	Asn	Asn	Thr	Glu	Asn	Asp	Asn	Ser	Gln
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Leu	Lys	Leu	Thr	Asn	Asn	Glu	Gln	Pro	Ser	Ala	Ala	Thr	Gln	Ala	Asn
	130					135					140				
Leu	Lys	Lys	Leu	Asn	Pro	Gln	Ala	Ala	Lys	Ala	Val	Gln	Asn	Ala	Lys
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Ile	Asp	Ala	Gly	Ser	Leu	Thr	Asp	Asp	Gln	Ile	Asn	Glu	Leu	Asn	Lys
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Ile	Asn	Phe	Ser	Lys	Ser	Ala	Glu	Lys	Gly	Ala	Lys	Leu	Thr	Phe	Lys
			180					185					190		
Asp	Leu	Glu	Gly	Ile	Gly	Asn	Ala	Ile	Val	Lys	Gln	Asp	Pro	Gln	Tyr
		195					200					205			
Ala	Ile	Pro	Tyr	Ser	Asn	Ala	Lys	Glu	Ile	Lys	Asn	Met	Pro	Ala	Thr

210	215	220																	
Tyr Thr Val Asp Ala Gln Thr Gly Lys Met Ala His Leu Asp Val Trp																			
225	230	235																	240
Asp Ser Trp Pro Val Gln Asp Pro Val Thr Gly Tyr Val Ser Asn Tyr																			
	245	250																	255
Met Gly Tyr Gln Leu Val Ile Ala Met Met Gly Ile Pro Asn Ser Pro																			
	260	265																	270
Thr Gly Asp Asn His Ile Tyr Leu Leu Tyr Asn Lys Tyr Gly Asp Asn																			
	275	280																	285
Asp Phe Ser His Trp Arg Asn Ala Gly Ser Ile Phe Gly Thr Lys Glu																			
	290	295																	300
Thr Asn Val Phe Gln Glu Trp Ser Gly Ser Ala Ile Val Asn Asp Asp																			
	305	310																	320
Gly Thr Ile Gln Leu Phe Phe Thr Ser Asn Asp Thr Ser Asp Tyr Lys																			
	325	330																	335
Leu Asn Asp Gln Arg Leu Ala Thr Ala Thr Leu Asn Leu Asn Val Asp																			
	340	345																	350
Asp Asn Gly Val Ser Ile Lys Ser Val Asp Asn Tyr Gln Val Leu Phe																			
	355	360																	365
Glu Gly Asp Gly Phe His Tyr Gln Thr Tyr Glu Gln Phe Ala Asn Gly																			
	370	375																	380
Lys Asp Arg Glu Asn Asp Asp Tyr Cys Leu Arg Asp Pro His Val Val																			
	385	390																	400
Gln Leu Glu Asn Gly Asp Arg Tyr Leu Val Phe Glu Ala Asn Thr Gly																			
	405	410																	415
Thr Glu Asp Tyr Gln Ser Asp Asp Gln Ile Tyr Asn Trp Ala Asn Tyr																			
	420	425																	430
Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Ser Phe Lys Leu Leu Asn																			
	435	440																	445
Asn Lys Lys Asp Arg Glu Leu Ala Gly Leu Ala Asn Gly Ala Leu Gly																			
	450	455																	460
Ile Leu Lys Leu Thr Asn Asn Gln Ser Lys Pro Lys Val Glu Glu Val																			
	465	470																	480
Tyr Ser Pro Leu Val Ser Thr Leu Met Ala Cys Asp Glu Val Xaa Xaa																			
	485	490																	495
Lys Leu Gly Asp Lys Tyr Tyr Leu Phe Ser Val Thr Arg Val Ser Arg																			
	500	505																	510
Gly Ser Asp Arg Glu Leu Thr Ala Lys Asp Asn Thr Ile Val Gly Asp																			

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Lys	Pro	Leu	Asn	Asn	Ser	Gly	Val	Val	Leu	Thr	Ala	Ser	Val	Pro	Ala
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Asn	Trp	Arg	Thr	Ala	Thr	Tyr	Ser	Tyr	Tyr	Ala	Val	Pro	Val	Ala	Gly
				565					570						575
His	Pro	Asp	Gln	Val	Leu	Ile	Thr	Ser	Tyr	Met	Ser	Asn	Lys	Asp	Phe
			580					585					590		
Ala	Ser	Gly	Glu	Gly	Asn	Tyr	Ala	Thr	Trp	Ala	Pro	Ser	Phe	Leu	Val
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Gln	Ile	Asn	Pro	Asp	Asp	Thr	Thr	Thr	Val	Leu	Ala	Arg	Ala	Thr	Asn
610						615					620				
Gln	Gly	Asp	Trp	Val	Trp	Asp	Asp	Ser	Ser	Arg	Asn	Asp	Asn	Met	Leu
625					630					635					640
Gly	Val	Leu	Lys	Glu	Gly	Ala	Ala	Asn	Ser	Ala	Ala	Leu	Pro	Gly	Glu
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Trp	Gly	Lys	Pro	Val	Asp	Trp	Ser	Leu	Ile	Asn	Arg	Ser	Pro	Gly	Leu
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Gly	Leu	Lys	Pro	His	Gln	Pro	Val	Gln	Pro	Lys	Ile	Asp	Gln	Pro	Asp
		675					680					685			
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690						695					700				
Asp	Lys	Pro	Ala	Gly	Lys	Ala	Thr	Pro	Asp	Asn	Thr	Asn	Ile	Asp	Pro
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Ser	Ala	Gln	Pro	Ser	Gly	Gln	Asn	Thr	Asn	Ile	Asp	Pro	Ser	Ala	Gln
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			740					745					750		
Gly	Lys	Asn	Thr	Asp	Ala	Lys	Gln	Leu	Pro	Gln	Thr	Gly	Asn	Lys	Ser
		755					760					765			
Gly	Leu	Ala	Gly	Leu	Tyr	Ala	Gly	Ser	Leu	Leu	Ala	Leu	Phe	Gly	Leu
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